WHAT IS CLAIMED IS:

1. A method for detection of at least one allele of a genetic locus comprising amplifying genomic DNA with an intron-spanning primer pair that defines a DNA sequence, said DNA sequence being in genetic linkage with said genetic locus and containing a sufficient number of intron sequence nucleotides to produce an amplified DNA sequence characteristic of said allele.

2. The method of Claim 1 wherein said amplified DNA sequence includes at least about 300 nucleotides corresponding to intron sequences.

3. The method of Claim 1 wherein said intron sequence is adjacent to an exon encoding said allele.

4. The method of Claim 1 wherein said amplified DNA sequence is characteristic of at least one nonadjacent allele.

5. The method of Claim 1 wherein said amplified DNA sequence is characteristic of at least one adjacent allele and at least one nonadjacent allele.

6. The method of Claim 5 wherein said amplified DNA sequence includes at least about 1,000 nucleotides corresponding to intron sequences.

7. A method for detection of at least one allele of a genetic locus comprising:

   a. amplifying genomic DNA with an intron-spanning primer pair that defines a DNA sequence, said DNA sequence being in genetic linkage with said allele and containing a sufficient number of intron sequence nucleotides to produce an amplified DNA sequence characteristic of said allele; and

b. analyzing said amplified DNA sequence to detect the presence of a genetic variation in said amplified sequence.

8. The method of Claim 7 wherein said variation in said amplified DNA sequence is a variation in the length of the primer-defined amplified DNA sequence.

9. The method of Claim 7 wherein said variation in said amplified DNA sequence is a change in the presence of at least one restriction site in the primer-defined amplified DNA sequence.

10. The method of Claim 7 wherein said variation in said amplified DNA sequence is a change in the location of at least one restriction site in the primer-defined amplified DNA sequence.

11. The method of Claim 7 wherein said variation in said amplified DNA sequence is a substitution of at least one nucleotide in the primer-defined amplified DNA sequence.

12. The method of Claim 7 wherein said genetic locus is a major histocompatibility locus.

13. The method of Claim 7 wherein said allele is associated with a monogenic disease.

14. The method of Claim 13 wherein said monogenic disease is cystic fibrosis.

15. The method of Claim 7 wherein at least about 70% of said primer-defined amplified DNA sequence corresponds to intron sequences.

16. The method of Claim 7 wherein said primer-defined amplified DNA sequence is from 300 to 500 nucleotides in length.

17. A method for producing RFLP fragments for an HLA locus of an individual comprising the steps of:

a. amplifying genomic HLA DNA from said individual with a primer pair specific for

said HLA locus under conditions suitable to produce an amplified DNA sequence; and

b. producing a digest by combining said amplified DNA sequence with at least one endonuclease that cleaves said amplified DNA sequence to yield a set of fragments having distinctive fragment lengths.

18. The method of Claim 17 additionally comprising the step of producing RFLP patterns from said digest.

19. The method of Claim 17 wherein said primers define a DNA sequence that contains all exons that encode allelic variability associated with said HLA locus.

20. A method for producing RFLP fragments for an HLA locus of an individual comprising the steps of:

a. amplifying genomic HLA DNA from said individual with a primer pair specific for said HLA locus under conditions suitable to produce an amplified DNA sequence, said primers defining a DNA sequence that contains all exons that encode allelic variability associated with said HLA locus; and

b. producing a digest by combining said amplified DNA sequence with at least one endonuclease that cleaves said amplified DNA sequence to yield a set of fragments having distinctive fragment lengths.

21. A method for producing RFLP patterns for an HLA locus of an individual comprising the steps of:

a. amplifying HLA DNA from said individual with a primer pair specific for said HLA locus under conditions suitable to produce an amplified DNA sequence, said primers being located in intervening sequence I and in intervening sequence III when said HLA locus is a Class I locus and in intervening

sequence I and in intervening sequence II when said locus is a Class II locus;

b. producing a digest by combining said amplified DNA sequence with at least one endonuclease that cleaves said amplified DNA sequence to yield a set of fragments having distinctive fragment lengths; and

c. producing RFLP patterns from said digest.

22. The method of Claim 21 wherein said amplification comprises:

a. combining an HLA-locus specific primer pair with HLA DNA from said individual under hybridizing conditions for a period of time sufficient for each primer in said primer pair to produce an extension product which, when separated from its complement, can serve as a template for synthesis of the extension product of the other primer to produce a mixture;

b. treating said mixture under denaturing conditions to separate the primers from their extension products;

c. treating said mixture with said HLA locus-specific primer pair such that a primer extension product is synthesized using each of the templates produced in step (b) as a template, resulting in amplification of the HLA DNA; and

d. repeating steps (b) and (c) to produce an amplified DNA sequence.

23. The method of Claim 21 wherein a second primer pair specific for said HLA locus is also used to amplify said HLA DNA.

24. The method of Claim 21 wherein producing said RFLP fragment pattern comprises:

a. combining said amplified DNA sequence with at least one endonuclease that cleaves said amplified DNA sequence to yield a set of fragments having distinctive fragment lengths;

b. separating said fragments based on the length of the fragments to produce separated fragments; and

c. visualizing said separated fragments to produce RFLP fragment patterns.

25. The method of Claim 24 wherein said fragments are separated using gel electrophoresis and visualized using a nucleotide-specific stain.

26. A method for determining whether DNA in a sample is from a particular individual comprising the steps of:

a. amplifying DNA from said individual and DNA from said sample with a primer pair specific for an HLA locus under suitable conditions to produce an amplified DNA sequence from said individual and from said sample, said primers being located in intervening sequences I and III for an HLA Class I locus and in intervening sequences I and II for a Class II locus;

b. combining said amplified DNA sequence from said individual and said amplified sample DNA from said sample with at least one endonuclease that cleaves said amplified DNA sequence into a plurality of cleaved sequences of sufficiently different lengths to distinguish between alleles of said HLA locus for a period of time sufficient for digestion of said amplified DNA to produce a digest; and

c. comparing restriction fragment length polymorphic patterns produced by said digest from said individual and from said sample.

27. A method for determining whether an individual is the father of a child comprising the steps of:

a. amplifying DNA from said individual, DNA from said child and DNA from said child's mother with a pair of primers specific for an HLA locus under suitable conditions to produce amplified DNA sequences, said primers being located in intervening sequences I and III for an HLA Class I locus and in intervening sequences I and II for a Class II locus;

b. combining said amplified DNA sequence from said individual and said amplified sample DNA from said child with at least one endonuclease that cleaves said amplified DNA sequence into a plurality of cleaved sequences of sufficiently different lengths to distinguish between alleles of said HLA locus to produce a digest; and

c. comparing restriction fragment length polymorphic patterns produced by said digest from said individual, from said child's mother and from said child.

28. An HLA locus-specific primer selected from the group consisting of a Class I locus-specific primer, a Class I A locus-specific primer, a Class I B locus-specific primer and a Class I C locus-specific primer.

29. The HLA locus-specific primer of Claim 28 wherein said primer has a sequence corresponding to at least 15 consecutive nucleotides selected from the group consisting of CATGTGGCCATCTTGAGAATGGA; GCCCGGGAGATCTACAGGCGATCA; CGCCTCCCTGATCGCCTGTAG; CCAGAGAGTGACTCTGAGG; CACAATTAAGGGAT;

TCCCCGGCGACCTATAGGAGATGG; CTAGGACCACCCATGTGACCAGC;
ATCTCCTCAGACGCCGAGATGCGTCAC;
CTCCTGCTGCTCTGGGGGGCAG; ACTTTACCTCCACTCAGATCAGGAG;
CGTCCAGGCTGGTGTCTGGGTTCTGTGCCCCT;
CTGGTCACATGGGTGGTCCTAGG;
CGCCTGAATTTTCTGACTCTTCCCAT;
ATCCCGGGAGATCTACAGGAGATG; AACAGCGCCCATGTGACCATCCT;
CTGGGGAGGCGCCGCGTTGAGGATTCT;
CGTCTCCGCAGTCCCGGTTCTAAAGTTCCCAGT;
ATCCTCGTGCTCTCGGGA; TGTGGTCAGGCTGCTGAC;
AAGGTTTGATTCCAGCTT;
CCCCTTCCCCACCCCAGGTGTTCCTGTCCATTCTTCAGGA;
CACATGGGCGCTGTTGGAGTGTCG; GTGAGTGCGGGGTCGGGAGGGA;
CACCCACCGGGACTCAGA; TGGCCCTGACCCAGACCTGGGC;
GAGGGTCGGGCGGGTCTCAGC; CTCTCAGGCCTTGTTC;
CAGAAGTCGCTGTTCC; TTCTGAGCCAGTCCTGAGA;
TTGCCCTGACCACCGTGATG; CTTCCTGCTTGTCATCTTCA;
CCATGAATTTGATGGAGA; ACCGCTGCTACCAATGGTA;
CCAAGAGGTCCCCAGATC; TCATCATAGCTGTGCTGATG;
AGAACATGTGATCATCCAGGC; CCAACTATACTCCGATCACCAAT;
TGACAGTGACACTGATGGTGCTG; GGGGACACCCGACCACGTTTC;
TGCAGACACAACTACGGGGTTG; TGGCTGAGGGCAGAGACTCTCCC;
TGCTACTTCACCAACGGGAC; GGTGTGCACACACAACTAC;
AGGTATTTTACCCAGGGACCAAGAGAT;
ATGTAAAATCAGCCCGACTGCCTCTTC;
GCCTCGTGCCTTATGCGTTTGCCTCCT;
TGAGGTTAATAAACTGGAGAA; GAGAGTGGCGCCTCCGCTCAT; and
GAGTGAGGGCTTTGGGCCGG.

30. An HLA Class I locus-specific primer pair.

31. An HLA Class II locus-specific, intron-spanning primer pair.

32. A DNA sequence defined by an HLA locus-specific primer pair.

33. A kit comprising at least one HLA locus-specific primer pair in a suitable container, wherein said HLA locus-specific primer pair is selected from

the group consisting of an HLA Class I locus-specific primer pair and an HLA Class II locus-specific, intron-spanning primer pair.

34. The kit of Claim 33 additionally comprising at least one endonuclease that cleaves a DNA sequence defined by said HLA locus-specific primer pair into a plurality of cleaved sequences of sufficiently different lengths to distinguish between alleles of said HLA locus.